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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/621,448DATE: 08/01/2000
TIME: 13:10:29Input Set : A:\seqlist- 1533 1010002.txt
Output Set : N:\CRF3\08012000\I621448.raw

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4 <110> APPLICANT: O'Donohue, Michael R.
5 Hanke, Paul D.
7 <120> TITLE OF INVENTION: Methods for Producing L-Amino Acids
9 <130> FILE REFERENCE: 1533.1010002
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/621,448
C--> 12 <141> CURRENT FILING DATE: 2000-07-21
14 <150> PRIOR APPLICATION NUMBER: 60/150,017
15 <151> PRIOR FILING DATE: 1999-08-20
17 <150> PRIOR APPLICATION NUMBER: 60/145,217
18 <151> PRIOR FILING DATE: 1999-07-23
20 <160> NUMBER OF SEQ ID NOS: 4
22 <170> SOFTWARE: PatentIn Ver. 2.1
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 1623
26 <212> TYPE: DNA
27 <213> ORGANISM: Corynebacterium glutamicum
29 <220> FEATURE:
30 <221> NAME/KEY: CDS
31 <222> LOCATION: (1)..(1620)
33 <400> SEQUENCE: 1
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35 Met Ala Asp Ile Ser Thr Thr Gln Ala Trp Gln Asp Leu Thr Asp His
36 1 5 10 15
38 tac tca aac ttc cag gca acc act ctg cgt gaa ctt ttc aag gaa gaa 96
39 Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
40 20 25 30
42 aac cgc gcc gag aag tac acc ttc tcc gcg gct ggc ctc cac gtc gac 144
43 Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
44 35 40 45
46 ctg tcg aag aat ctg ctt gac gac gcc acc ctc acc aag ctc ctt gca 192
47 Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
48 50 55 60
50 ctg acc gaa gaa tct ggc ctt cgc gaa cgc att gac gcg atg ttt gcc 240
51 Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
52 65 70 75 80
54 ggt gaa cac ctc aac acc gaa gac cgc gct gtc ctc cac acc gcg 288
55 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
56 85 90 95
58 ctg cgc ctt cct ccc gaa gct gat ctg tca gta gat ggc caa gat gtt 336
59 Leu Arg Leu Pro Pro Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
60 100 105 110
62 gct gct gat gtc cac gaa gtt ttg gga cgc atg cgt gac ttc gct act 384
63 Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
64 115 120 125
66 gcg ctg cgc tca ggc aac tgg ttg gga cac acc ggc cac acg atc aag 432
67 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
68 130 135 140

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70 aag atc gtc aac att ggt atc ggt ggc tct gac ctc gga cca gcc atg 480
71 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
72 145 150 155 160
74 gct acg aag gct ctg cgt gca tac gcg acc gct ggt atc tca gca gaa 528
75 Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
76 165 170 175
78 ttc gtc tcc aac gtc gac cca gca gac ctc gtt tct gtg ttg gaa gac 576
79 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
80 180 185 190
82 ctc gat gca gaa tcc aca ttg ttc gtg atc gct tcg aaa act ttt acc 624
83 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
84 195 200 205
86 acc cag gag acg ctg tct aac gct cgt gca gct cgt gct tgg ctg gta 672
87 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
88 210 215 220
90 gag aag ctc ggt gaa gag gct gtc gcg aag cat ttc gtc gca gtg tcc 720
91 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
92 225 230 235 240
94 acc aat gct gaa aag gtc gca gag ttc ggt atc gac acg gac aac atg 768
95 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
96 245 250 255
98 ttc ggc ttc tgg gac tgg gtc gga ggt cgt tac tcc gtg gac tcc gca 816
99 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
100 260 265 270
102 gtt ggt ctt tcc ctc atg gca gtg atc ggc cct cgc gac ttc atg cgt 864
103 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
104 275 280 285
106 ttc ctc ggt gga ttc cac gcg atg gat gaa cac ttc cgc acc acc aag 912
107 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
108 290 295 300
110 ttc gaa gag aac gtt cca atc ttg atg gct ctg ctc ggt gtc tgg tac 960
111 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
112 305 310 315 320
114 tcc gat ttc tat ggt gca gaa acc cac gct gtc cta cct tat tcc gag 1008
115 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
116 325 330 335
118 gat ctc agc cgt ttt gct gct tac ctc cag cag ctg acc atg gaa tca 1056
119 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
120 340 345 350
122 aac ggc aag tca gtc cac cgc gac ggc tcc cct gtt tcc act ggc act 1104
123 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
124 355 360 365
126 ggc gaa att tac tgg ggt gag cct ggc aca aat ggc cag cac gct ttc 1152
127 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
128 370 375 380
130 ttc cag ctg atc cac cag ggc act cgc ctt gtt cca gct gat ttc att 1200
131 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
132 385 390 395 400
134 ggt ttc gct cgt cca aag cag gat ctt cct gcc ggt gag cgc acc atg 1248

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135 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
136          405          410          415
138 cat gac ctt ttg atg agc aac ttc ttc gca cag acc aag gtt ttg gct 1296
139 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
140          420          425          430
142 ttc ggt aag aac gct gaa gag atc gct gcg gaa ggt gtc gca cct gag 1344
143 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
144          435          440          445
146 ctg gtc aac cac aag gtc atg cca ggt aat cgc cca acc acc att 1392
147 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
148          450          455          460
150 ttg gcg gag gaa ctt acc cct tct att ctc ggt gcg ttg atc gct ttg 1440
151 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
152 465          470          475          480
154 tac gaa cac atc gtg atg gtt cag ggc gtg att tgg gac atc aac tcc 1488
155 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
156          485          490          495
158 ttc gac caa tgg ggt gtt gaa ctg ggc aaa cag cag gca aat gac ctc 1536
159 Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
160          500          505          510
162 gct ccg gct gtc tct ggt gaa gag gat gtt gac tcg gga gat tct tcc 1584
163 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
164          515          520          525
166 act gat tca ctg att aag tgg tac cgc gca aat agg tag 1623
167 Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
168          530          535          540
171 <210> SEQ ID NO: 2
172 <211> LENGTH: 540
173 <212> TYPE: PRT
174 <213> ORGANISM: Corynebacterium glutamicum
176 <400> SEQUENCE: 2
177 Met Ala Asp Ile Ser Thr Thr Gln Ala Trp Gln Asp Leu Thr Asp His
178 1          5          10          15
180 Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
181          20          25          30
183 Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
184          35          40          45
186 Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
187          50          55          60
189 Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
190 65          70          75          80
192 Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
193          85          90          95
195 Leu Arg Leu Pro Pro Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
196          100          105          110
198 Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
199          115          120          125
201 Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
202          130          135          140

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204 Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
205 145 150 155 160
207 Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
208 165 170 175
210 Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
211 180 185 190
213 Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
214 195 200 205
216 Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
217 210 215 220
219 Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
220 225 230 235 240
222 Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
223 245 250 255
225 Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
226 260 265 270
228 Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
229 275 280 285
231 Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
232 290 295 300
234 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
235 305 310 315 320
237 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
238 325 330 335
240 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
241 340 345 350
243 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
244 355 360 365
246 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
247 370 375 380
249 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
250 385 390 395 400
252 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
253 405 410 415
255 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
256 420 425 430
258 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
259 435 440 445
261 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
262 450 455 460
264 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
265 465 470 475 480
267 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
268 485 490 495
270 Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
271 500 505 510
273 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
274 515 520 525
276 Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg

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277      530      535      540
281 <210> SEQ ID NO: 3
282 <211> LENGTH: 25
283 <212> TYPE: DNA
284 <213> ORGANISM: Corynebacterium glutamicum
286 <400> SEQUENCE: 3
287 gctgatgtcc acgaagcttt gggac 25
290 <210> SEQ ID NO: 4
291 <211> LENGTH: 25
292 <212> TYPE: DNA
293 <213> ORGANISM: Corynebacterium glutamicum
295 <400> SEQUENCE: 4
296 gctgagaacc ttggaataag gtagg 25
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VERIFICATION SUMMARY DATE: 08/01/2000
PATENT APPLICATION: US/09/621,448 TIME: 13:10:30

Input Set : A:\seqlist- 1533 1010002.txt
Output Set: N:\CRF3\08012000\I621448.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date